

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and  
Amino Acid Sequence (SEQ ID NO: 2)

(Agp-96614-a1)

(CD20RP2)

5

1	TTCCAGTGCTCCAGGCAGCCTCAGCACAAGAAAAGAACATGGTCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGCACCGCACACAG	120
1	M D S S T A H S	8
121	TCCGGTGTCTTCTGGTATTTCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAAAAATTATTTGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCCTGTTTGGGAATTATGACCTTTCTTTTGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTTCACTTTGTATAAACCATATCCAAGGTTTCCCTTTATATTTCTTTTCAGGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTTTGTTCATTAATTCTGGAGCCTTCCTAATTGCAGTGAAAAGAAA	420
89	F W G S V L F I N S G A F L I A V K R K	108
421	AACCACAGAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGTGCCCTGGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTCTCCTCACATTTGGTTTCATCCTAGATCAAACTACATTTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C G	148
541	TTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTTGGAATTTTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGATGACTTTTCAGCATTATTGAATTATTCATTTCTCTGCCTTTCTCAATTTTGGG	660
169	T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	760

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and  
Amino Acid Sequence (SEQ ID NO: 4)  
(Agp-69406-a1)  
(CD20RP1)

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1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
61	GCCACAGCACACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC	120
1		5
	M L L Q S	
121	CCAAACCATGGGGGTTTCTCACAGCTTTACACCAAAGGGCATCACTATCCCTCAAAGAGA	180
6	Q T M G V S H S F T P K G I T I P Q R E	25
181	GAAACCTGGACACATGTACCAAACGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC	240
26	K P G H M Y Q N E D Y L Q N G L P T E T	45
241	CACCGTTCTTGGGACTGTCCAGATCCTGTGTTGCCTGTTGATTTCAGTCTGGGGGCCAT	300
46	T V L G T V Q I L C C L L I S S L G A I	65
301	CTTGGTTTTTGTCTCCCTACCCCTCCCACTTCAATCCAGCAATTCCACCACTTTGATGTC	360
66	L V F A P Y P S H F N P A I S T T L M S	85
361	TGGGTACCCATTTTATAGGAGCTCTGTGTTTTGGCATTACTGGATCCCTCTCAATTATCTC	420
86	G Y P F L G A L C F G I T G S L S I I S	105
421	TGGAAAACAATCAACTAAGCCCTTTGACCTGAGCAGCTTGACCTCAAATGCAGTGAGTTC	480
106	G K Q S T K P F D L S S L T S N A V S S	125
481	TGTTACTGCAGGAGCAGGCCTCTTCCTCCTTGCTGACAGCATGGTAGCCCTGAGGACTGC	540
126	V T A G A G L F L L A D S M V A L R T A	145
541	CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTCGCTTATTCGGAGTACTA	600
146	S Q H C G S E M D Y L S S L P Y S E Y Y	165
601	TTATCCAATATATGAAATCAAAGATTGTCTCCTGACCAGTGTCAGTTTAACAGGTGTCCT	660
166	Y P I Y E I K D C L L T S V S L T G V L	185
661	AGTGGTGATGCTCATCTTCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTT	720
186	V V M L I F T V L E L L L A A Y S S V F	205
721	TTGGTGGAACAGCTCTACTCCAACAACCCTGGGAGTTCATTTTCCTCGACCCAGTCACA	780
206	W W K Q L Y S N N P G S S F S S T Q S Q	225
781	AGATCATATCCAACAGGTCAAAAAGAGTTCTTCACGGTCTTGGATATAAGTAACTCTTGG	840
226	D H I Q Q V K K S S S R S W I *	241
841	CCTCAGAGGAAGGAAAAGCAACTCAACACTCATGGTCAAGTGTGATTAGACTTTCTGAA	900
901	ATCTCTGCCATTTTATAGATACTGTGAAACAACTAAAAAAAAAAGCTTTTGTTTTGTATTT	960
961	GAAAAAAAAAAAAAAAAAAAAA	982



hTMM	.....ASH E	VON.....ABL G	SASA.....	HGTGSET O	EEL-NH.....S	32
h GERB	HAGYSHOR	PEE.....STS	AMHTNMG	QWPGAGU	POLGHH.....A	44
HURP4	.....TSOPH	PH.....TII Y	LPS.....	WNI FSOAK	PG.....P	29
94006	.....LLQSG	THG.....VSH	FTP.....	KG TI POBK	PG.....H	29
1 qERbat o	.....TE SHR	RAN.....LAL P	QEPSSVAF	EVLEI SQEV	SSGRLL.....K	40
96614	.....DSTSA	HSP.....VFL Y	FPF.....	-E I TASEY	TEL-SA.....T	31
HTPEF86	MHSVSAVP	ANSULVAPH	NGV PV TGI M	SHVPL VYMS	POU HV RGNP	50
hCD20	MTFPHSV	.....N	GTF PAEP-MK	GPI AHSGSK	P.....LF R PH	34
HTMMSF5	MDTGQA	.....N	ROGL	.....	.....	12
HTAL6	MDVQGA	.....	ROI GH	.....	.....	12
Conf enz w	M.....	.....	.....	.....	.....	50
hTMM	VYHPI.....NES	QD-YOKALR	VILGA Q LNA	MYLALGIML	QSL QV WYFO	79
h GERB	VI HSHWKQ	GVTI KGEKP	VILGVU Q LTA	UMLSGH	PMH-SNI YG	93
HURP4	THQSG.....DSL	KQ-HLHAB K	VIGTI Q UOG	MYLSGL	ASATSRHT	76
94006	MYQIE.....DYL	QN-GL PETT	VILGTI Q LCO	LII SSLGL	VFAVPPSHFN	76
1 qERbat o	SASSPLHW	LT-QL KHEC	FLGVT Q LTA	M CLOFQW	QSVLDI SH E	88
96614	FTI STQ-SPL	QK-LF ARMK	ILGTI Q LFG	IMTFSFGV	LFTL-LHPYF	77
HTPEF86	PSLVSYNHG	PYOKALKBK	TILGA Q I I G	LAM GLGSI M	ATV-LVGEVL	79
hCD20	SSLVG-PHQ	TF-FMREK	TILGA Q MNG	LIL ALGGL	MYL-VGEV YA	98
HTMMSF5	SLIG	.....L	QYCI-VANA	LLVFNK	-TSW TM-N	41
HTAL6	-SLVT	.....L	ALLO-HAHN	LLVFNK	-TKY-ASE-N	41
Conf enz w	.....	.....E	LG-I Q U	L.....G	.....	100
hTMM	KHFFIFTFYI	GPI WGAUW	CSGSI LSWA	G KP	.....T	114
h GERB	SNFI.....PI SVVI	GVTI WGSUM	II SGLS LA	G RT	.....T	126
HURP4	QV-TSTILNS	APFI GFPT	II SGLS AT	ENPL	.....T	110
94006	PA-I STILMS	GVPFL GAIQ	II SGLS I S	QKOS	.....T	110
1 qERbat o	GD-I FESSKA	GVPFWGAIFF	II SGLS I S	EPKNT	.....A	123
96614	R-PPFI FLS	GVPFWGVL	II SGLS LA	ENK	.....T	110
HTPEF86	PI SYVGV	PF-W GGLW	II SGLSVA	ENK	.....YS	126
hCD20	PI OTYVWV	PL-W GQIM	II SGLSLAT	ENK	.....P	121
HTMMSF5	HL SLOWWHL	GR-G GGLSW	LOFG AWFA	QKOSQSG	QGN.....RC	88
HTAL6	HL SVPVWFS	G-VGGLIM	LLRWF VI G	EQQDQO-Q	QSHENGKRC	88
Conf enz w	.....	QV.....G L F	II SGLS LA	.....	.....	150
hTMM	.....	.....FTW	I QHST GMIT	SATI ALVGT	FLSLN AVN	147
h GERB	.....	.....KEL	VRSLS GMIT	SVLWASGL	I NTSLS FY-Y	158
HURP4	.....	.....MLL	VHSL VOSL	SALSALVGI	LSVQWMLN	143
94006	.....	.....MPF	DLSSL TSNV	SVYTAGGLF	LLADSHALR	143
1 qERbat o	.....	.....TYL	VRSLS GMIT	SVS AGGITG	ILI I NLMKSL	151
96614	.....	.....ETL	ILI SRIMPT	SALGAI AGI	LLTFGLDQ	154
HTPEF86	.....	.....VCL	LSGL GNVY	SVS AGGITG	LLTFGLDQ	144
hCD20	.....	.....KOL	VRSLS GMIT	SVS AGGITG	LLTFGLDQ	154
HTMMSF5	.....	.....PMLRSV SSA	QVULGA VCL	SVS AGGITG	LLTFGLDQ	154
HTAL6	.....	.....RMLSSV LAL	I G AGSVCY	SVS AGGITG	LLTFGLDQ	154
Conf enz w	.....	.....L	.....	.....	.....	200
hTMM	QSLRSCHSS	E.....SPILC	NVMSG.....I	SN.....	-GMYSL-LI	179
h GERB	-SPH-MHSS	-P-YC	NYGN.....S	NNOHTHEIL	MLDGM-LI	190
HURP4	PASQOGLK	H-N PTRSV	SVYVHDS VT	TDCT AKAS	AGI LSL M LI	191
94006	TASQOGLK	D-VLSL PVS	EYVYV-YEI	TCOLTSV SL	TSI LVHML LI	190
1 qERbat o	AVI H.....	I HSOQ	KFF.....E	TQFMAF S	TEI VVHML LI	187
96614	WI H.....	-O	QSHR.....N	SOOKA.....	VTVLFLG LI	187
HTPEF86	IPH.....	PH.....AP	QVY.....	P.....Y	ANGVNP M R	163
hCD20	I SHVLMESL	HFI RAH PI	W YNDPAP	SEKNSPST	QYSI QSLU LG	192
HTMMSF5	TAG.....	WILLNRI LND	ROE.....	GFV.....	PRVVPVNI VT	157
HTAL6	TEG.....	QWLDYS WS	ECF.....	.....E P	KH VEWV VS	161
Conf enz w	.....	.....	.....Y.....	.....	.....L	250
hTMM	LTLLLECVTI	STI AM	.....WCM	.....ANQNS	.....GMYSL-LI	179
h GERB	LSVLEFCI AV	LSAF	.....GOK	.....VL OCT-P	GGV VLI LPSH	223
HURP4	QCTLEFCI AV	LTAVL	.....PMK	.....QVSDFP	QSGV LFL RST	224
94006	FTVLELL LAA	TSVYF	.....WIK	.....GLTSNP	GGSTLSST	224
1 qERbat o	LTILLGQSV	SLTI C	.....GAG	.....EELYSK	VPE DRYEEL	232
96614	LTILVFSILE	LFI SL	.....PT S	.....I LGOH	.....	190
HTPEF86	LSGILLVFL	LEFG	.....AGAS	SHFQGLV OG	.....QSNV	217
hCD20	LF SVLMI FAF	FOELV IAG V	ENE WKPCSS	PKSH VLL SA	EKKKGTI NI	242
HTMMSF5	IL SHYLAAGC	LGLV V	.....C	G GLV	.....NAT I	182
HTAL6	LF SI LLALGG	LEF I L	.....C	.....LI QW	.....NGVL	186
Conf enz w	.....L L	.....	.....C	.....	.....	300
hTMM	.....	.....	.....	.....	.....	214
h GERB	.....	.....	.....	.....	.....	239
HURP4	.....	.....	.....	.....	.....	248
94006	.....	.....	.....	.....	.....	240
1 qERbat o	.....	.....	.....	.....	.....	240
96614	.....	.....	.....	.....	.....	244
HTPEF86	.....	.....	.....	.....	.....	200
hCD20	.....	.....	.....	.....	.....	245
HTMMSF5	.....	.....	.....	.....	.....	292
HTAL6	.....	.....	.....	.....	.....	193
Conf enz w	.....	.....	.....	.....	.....	197
hTMM	.....	.....	.....	.....	.....	214
h GERB	.....	.....	.....	.....	.....	239
HURP4	.....	.....	.....	.....	.....	248
94006	.....	.....	.....	.....	.....	240
1 qERbat o	.....	.....	.....	.....	.....	240
96614	.....	.....	.....	.....	.....	244
HTPEF86	.....	.....	.....	.....	.....	200
hCD20	.....	.....	.....	.....	.....	245
HTMMSF5	.....	.....	.....	.....	.....	292
HTAL6	.....	.....	.....	.....	.....	193
Conf enz w	.....	.....	.....	.....	.....	197
hTMM	.....	.....	.....	.....	.....	214
h GERB	.....	.....	.....	.....	.....	239
HURP4	.....	.....	.....	.....	.....	248
94006	.....	.....	.....	.....	.....	240
1 qERbat o	.....	.....	.....	.....	.....	240
96614	.....	.....	.....	.....	.....	244
HTPEF86	.....	.....	.....	.....	.....	200
hCD20	.....	.....	.....	.....	.....	245
HTMMSF5	.....	.....	.....	.....	.....	292
HTAL6	.....	.....	.....	.....	.....	193
Conf enz w	.....	.....	.....	.....	.....	197